Interpretable classification of complex collective motions using graph dynamic mode decomposition

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Abstract

Understanding biological network dynamics is a fundamental issue in various scientific and engineering fields. Here we introduced a data-driven spectral analysis called graph dynamic mode decomposition, which obtains the dynamical properties for collective motion classification. Using a ballgame as an example, we classified the strategic collective motions in different global behaviors and discovered the label-specific stronger spectra in the relationship among the nearest agents, providing physical and semantic interpretations. Our approach contributes to the understanding of principles of biological complex network dynamics from the perspective of nonlinear dynamical systems.

Keywords: Dynamical systems, Dynamic mode decomposition, Sports

1. Introduction

Our motivation is to understand the principles of network dynamics of biological complex collective motions by directly extracting the dynamical properties of the network in a data-driven manner. As a method of describing nonlinear dynamical systems with a global mode by the direct extraction of dynamical properties, operator-theoretic approaches such as the Koopman operator (Koopman, 1931) have attracted attention in fields such as applied mathematics, physics and machine learning. One of the most popular algorithms for spectral analysis of the Koopman operator is dynamic mode decomposition (DMD)(Rowley et al., 2009; Schmid, 2010). Among several variants of DMDs, Graph DMD (Fujii and Kawahara, 2019; Fujii et al., 2019) can extract and visualise the underlying low-dimensional global dynamics of graph dynamical systems (GDSs) with structures among observables from data. For the related works, see (Fujii and Kawahara, 2019).

2. Graph DMD

First, we consider an autonomous discrete-time weighted and undirected GDS described using an adjacency matrix $\boldsymbol{A}_t \in \mathbb{R}^{m \times m}$, whose element represents the weight on the rela-

tionship between components (e.g., agents) at each time t (for details, see (Fujii et al., 2019)). For the practical implementation of Koopman spectral analysis with dependent structure among observables (Fujii et al., 2019), a modified tensor-based DMD (Fujii and Kawahara, 2019) is applied to the adjacency matrix series. In summary, a sequence of adjacency matrices is decomposed into spatial coefficients and temporal dynamics: $\boldsymbol{A}_t \approx \sum_{j=1}^{p} \boldsymbol{Z}_j \hat{\lambda}_j^t b_{j,0}$, where λ_j called Graph DMD eigenvalue characterises the time evolution, i.e., the phase of λ_j determines its frequency and the magnitude determines the growth rate of its dynamics, $\boldsymbol{Z}_j \in \mathbb{C}^{m \times m}$ is the spatial coefficients called Graph DMD modes, and $b_{j,0}$ works as an initial value.

3. Experiments and conclusion

Using a basketball game as an example, we classified the strategic collective motions in different global behaviors and discovered the label-specific stronger spectra in the relationship among the nearest agents, providing physical and semantic interpretations (for the detail, see (Fujii et al., 2019)). Our approach contributes to the understanding of principles of biological complex network dynamics from the perspective of nonlinear dynamical systems.

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